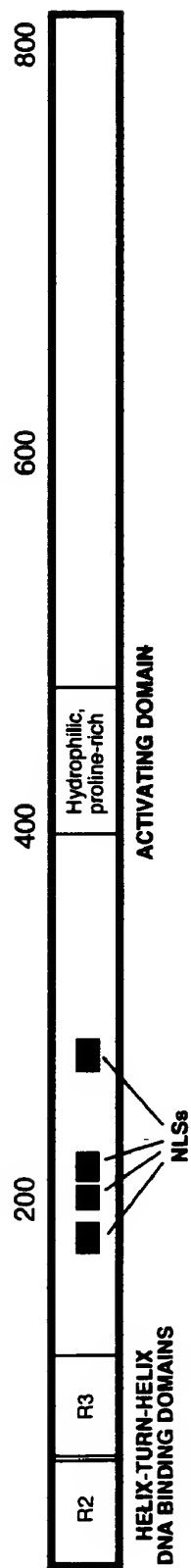
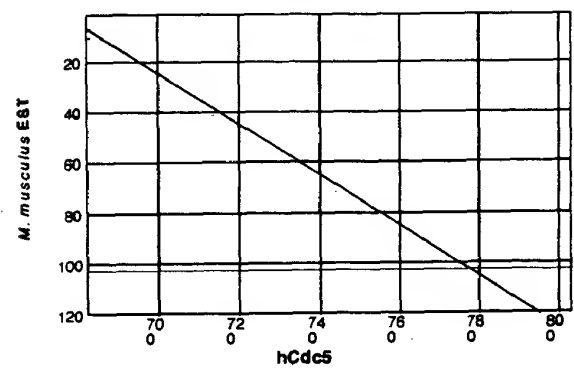
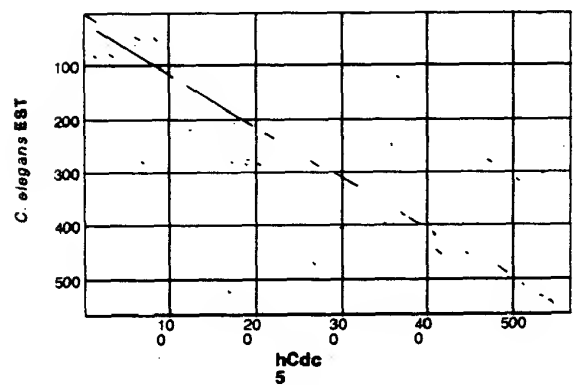
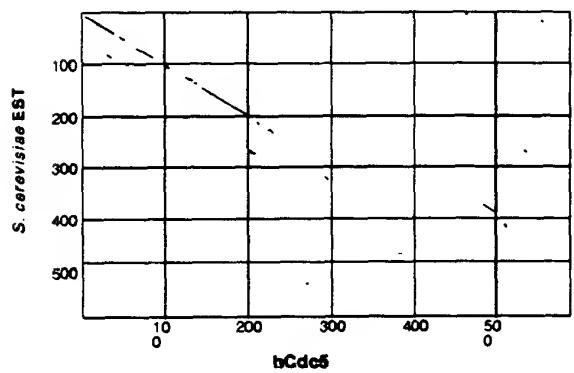
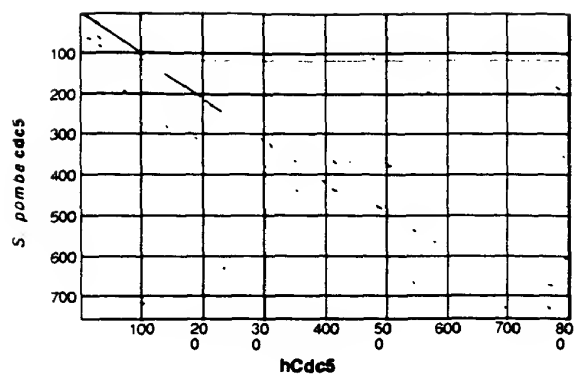


MPRIMIKGGVWRNTEDEILKAAVMKYGKNQWSRIASLLHRKSAKQCKARW 50  
 YEWLDPSIKKTEWSREEEEKLLHLAKLMPTQWRTIAPIIGRTAAQCLEHY 100  
 EFLLDKAAQRDNEEETTDDPRKLKPGEIDPNPETKPARPDPIDMDEDELE 150  
 MLSEARARLANTQGGKAKRKAREKQLEEARRLAALQKRRELRAAGIEIQK 200  
 KRKRKRGVDYNAEIPFEKKPALGFYDTSEENYQALDADFRKLRQQDLGGE 250  
 LRSEKEGRDRKKDKOHLKRKESDLPSAILQTSGVSEFTKKRSKLVLPAP 300  
 QISDAELQEVVKVGQASEIARQTAEESGITNSASSTLLSEYNVTNNSVAL 350  
 RTPRTPASQDRILQEAQNLMAITNVDTPKGGGLNTPLHESDFSGVTPORO 400  
 VVQTPNTVLSTPFRTPSNGAEGLTTPRSGTTPKPVINSTPGRTPLRDKLNI 450  
 NPEDGMADYSDPSYVKOMERESREHLRLGLLGLPAPKNDFEIVLPENAEK 500  
 ELEEREIDDTYIEDAADVDARKQAIRDAERVKEMKRMHKAVQKDLPRPSE 550  
 VNETILRPLNVEPPLTDLQKSEELIKKEMITMLHYDLLHHPYEPSGNKKG 600  
 KTVGFGTNNSEHITYLEHNPYEKFSKEELKKAQDVLVQEMEVVKQGMSHG 650  
 ELSSEAYNQVWEECYSQLYLPGQSRYTRANLASKKDRIESLEKRLEINR 700  
 GHMTTEAKRAAKMEKKMKILLGGYQSRAMGLMKQLNDLWDQIEQAHLER 750  
 TFEELKKHEDSAIPRRLECLKEDVQRQQEREKELQHRYADLLLEKETLKS 800  
 KF\*

Fig. 1A



**Fig. 1B**



**Fig. 2A**

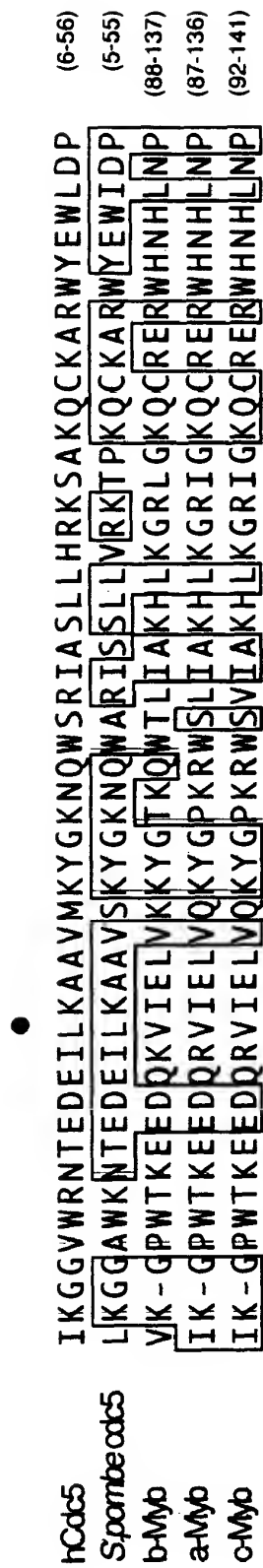


Fig. 2B

hCdc5	PLKGGGLNTPLHESDFSGVTPQRQVVQTPNTVLSTPFRTPSNGAEGLTPRSGLTPKPVINSTP (378-439)
<i>S. pombe</i> cdc5	SVTIEVRNQLMNREQSSLLGQESIPLQPGGTGYTGVTPSHAANGS---ALAAP--Q--ATP (380-434)
b-Myb	PVK-TL--PFSPSQFLNFWNKQDTLEESPSLTSTPVCSQKVVTTPPLHRDKTPLHQKHAAF (445-503)
a-Myb	ILRKKRKMVRVGHSPGSEL-RDGSUNDGGNMALKTPLKTPFSPSQFFNTCPGNEQLNIENPSF (446-508)
hCdc5	GRTPLRDKLNIINPEDGMADYSDPSYVKQMERESREHLRLGLLPAPKNDFEIVLPENAEK (440-500)
<i>S. pombe</i> cdc5	FRTPR-DTFSINAAERAGR-LASE-REN-KIRLKALRELLAKLPKPNKYEL-ME-P-R- (435-487)
b-Myb	VTPDQKYSMDNTRHTP-TPFKNAKYGPKLPQTPHLEEDLKEVLRSEAGIELIIEDDIRP (504-565)
a-Myb	TSTPICGQKAL-ITTPLHKETTPKDQKENVGFRTPTIRRSILGTPTPTPFKNALAAQEKK (509-569)

Fig. 2C

5' untranslated region:

GGCAGGAGAGGAAGTGGCGGCTTTGAGTCCGGTGGCCCAATCGCTGTTACTACTTCTCTGAAGCTCCTCTCGGCTGCTTGC  
CGAGACACCCCTGCCCAAG

Coding region:

1 DNA BINDING DOMAIN (\_\_\_)

1 atgcctcga ttatgatcaa ggggggcgta tggaggaata ccgaggatga aattctgaaa  
61 gcagcggtaa tgaatatatg gaaaaatcag tggctcatt cctgcataga  
121 aatcagcaa agcaatgcaa agccagatg targaatggc tggatccaaq cattaagaaq  
181 acagaatggt ccagagaaga agaggaaaaa ctcttgactc tggccaagtt gatgccaact  
241 cagtggagga ccattgctcc aatcattgga agaacagcgg cccagtgctt agaacactat  
301 gaatttcttc tggataaagc tgcccaaaga gacaatgaag aggaacaac agatgatcca  
361 cgaaaactta aacctggaga aatagatcca aatccagaaa caaaaccagc gcggcctgat  
421 ccaattgata tggatgagga tgaacttgag atgctttctg aagccagagc ccgcttggt

2 NUCLEAR LOCALIZATION DOMAIN (....)

481 aatactcagg gaaagaaggc caagaggaaa gcaagagaga aacaattgga agaagcaaga  
541 cgtcttgctg ccctccaaaa aagaagagaa ctctgagcag ctggcataga aattcagaag  
601 aaaagaaaaa ggaagagaggy agttgattat aatgcccga tccattttga aaaaagcct  
661 gccccttggt tttatgatag ttctgaggaa aactaccaag ctcttgacgc agatttcagg  
721 aatlaagac aacagatctt tgatggggag ctatgatctg aaaaagaagg aagagataga  
781 aaaaagaca aacagcattt gaaaaggaaa aaagaatctg attaccatc agctattctt  
841 caaactagt gtgtttctga attactaaa aagagaagca aactagtact tctgcccct  
901 cagatttcag atgcagaact ccaggaagtt gtaaaagtag gccaaagcag tgaattgga  
961 cgtcaactg ccgaggaatc tggcataaca aattctgctt ccagtacact tttgtctgag  
1021 tacaatgtca ccaacaacag cgttgctctt agaacaccac gaacaccagc ttcccaggac  
1081 agaattctgc aggaagcca gaacctcatg gccctacca atgtggacac cccattgaaa

3 ACTIVATING DOMAIN (\_\_\_)

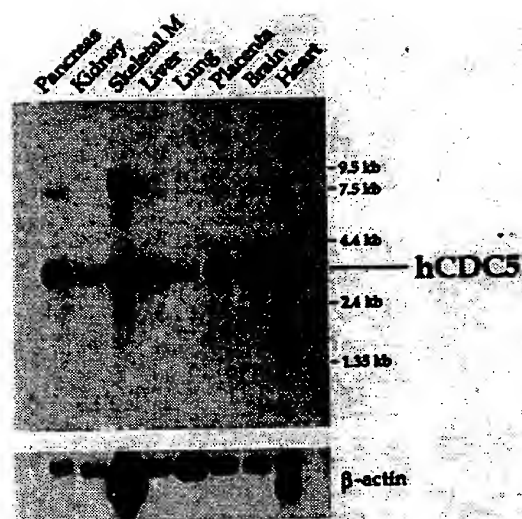
1141 ggtggactta ataccccat gcatgagagt gacttctcag gtgtaactcc acagcgacaa  
1201 gttgtagaga ctccaaacac agttctctct actccattca ggaactcctc taatggagct  
1261 gaagggctga ctccccggag tggaaacaact cccaaaccag ttattaactc tactccgggt  
1321 agaactcctc ttcgagacaa gttaaacatt aatccccgag atggaatggc agactatagt  
1381 gatccctctt acgtgaagca gatggaaaaga gaatccccgag aacatctccg tttagggttg  
1441 ttgggccttc ctgcccctaa gaatgatttt gaaattgttc taccagaaaa tgcgagaag  
1501 gagctggaag aacgtgaaat agatgatact tacattgaag atgctgctga tgtggatgct  
1561 cgaaagcagg ccatacgaga tgcagagcgt gtaaaaggaaa tgaacgaat gcataaagct  
1621 gtccagaaag atctgccaag accatcagaa gtaaatgaaa ctattctaag acccttaa  
1681 gtagaaccgc ctttaacaga tttacagaaa agtgaagaac taatcaaaaa agaatgatc  
1741 acaatgcttc attatgacct tctacatcac ccttatgaac catctggaaa taaaaaggc  
1801 aaaactgtag ggtttggtac caataattca gagcacatta cctatctgga acataatcct  
1861 tatgaaaagt tctccaaaga agagctgaaa aaggcccagg atgttttggt gcaggagatg  
1921 gaagtgggta aacaaggaat gagccatgga gagctctcaa gtgaagctta taaccagggtg  
1981 tgggaagaat gctacagtca agttttatat ctctctgggc agagccgcta cacacggg  
2041 aatctggcta gtaaaaagga cagaattgaa tcaactgaaa agaggctcga gataaacagg  
2101 ggtcacatga cgacagaagc caagagggct gcaaatgatg aaaagaagat gaaaattttg  
2161 cttggggggt accagtctcg tgctatgggg ctcatgaaac agttgaatga cttatgggac  
2221 caaattgaac aggtcactt ggagttacgc acttttgaag aactcaagaa acatgaagat  
2281 tctgctattc cccggaggct agagtgtcta aaagaagacg ttcagcgaca acaagaaaga  
2341 gaaaaggaac ttcaacatag atatgctgat ttgctgctgg agaaagagac tttaaagtca  
2401 aaattctga

3' untranslated region:

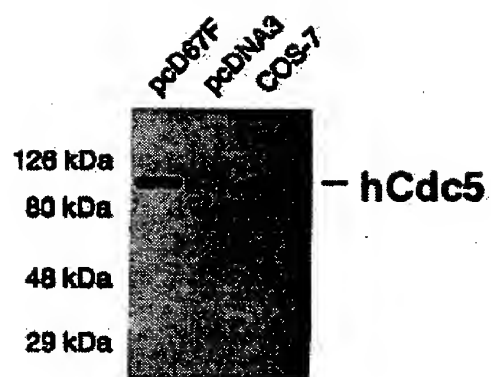
AGTACAGTTTATATCTGTACAGGATTAAATTAATGCGGTTTTCATACTCTAGAAGGCTGAAACTG ATGTTTATCTTCATTGACA  
AATTTACCCACCACTGTGCTTTTTCAGTTGTTTATTTTAAATGATATCGATCTTACACATTCTGTGTATAAAGACCTTAACCTCACA  
GGACGGACATTTTAGAGTTTAAATTATTA AGGCTATCATCTTTTAGTAATGTCATATTTGCCAACTTTTTTAGTTTGGCCTTTAA  
TTTAAAAAGCCTAATTTTAAAGTGCTGCCGTGTGAGTAACTCTTGAATAAAAAACAAATATAAAAA

Fig. 2D

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**FIG. 3**



**FIG. 4A**

09757049 040804  
T08070 64025260



**FIG. 4B**

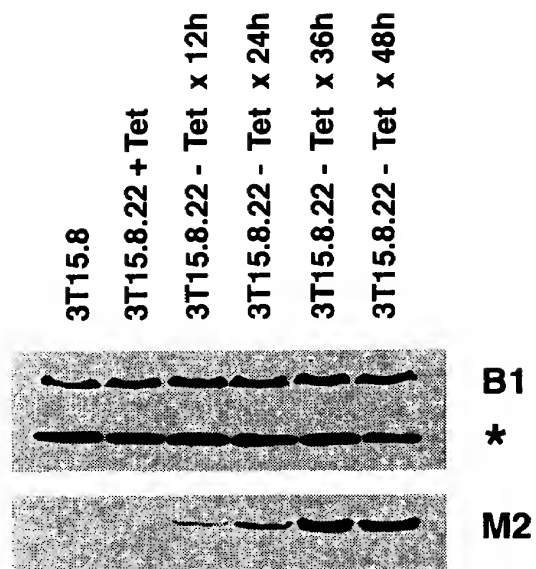
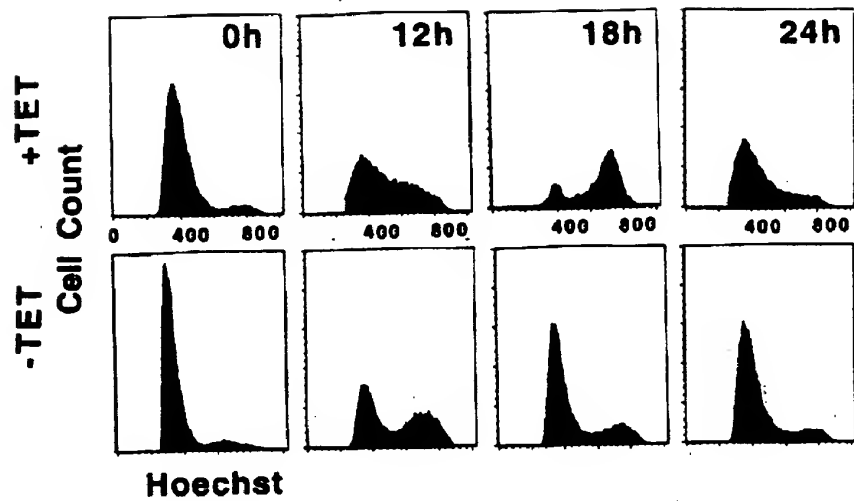


FIG. 5



**Fig. 6**

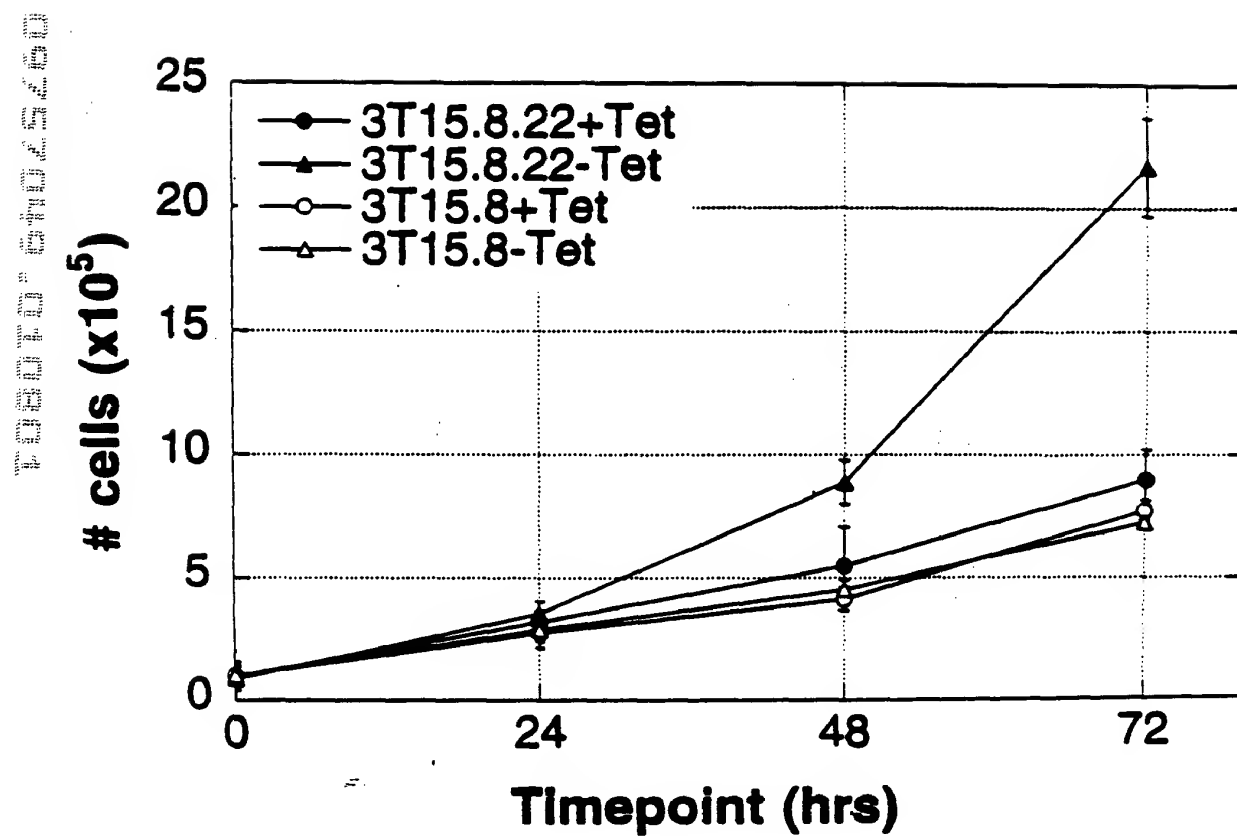
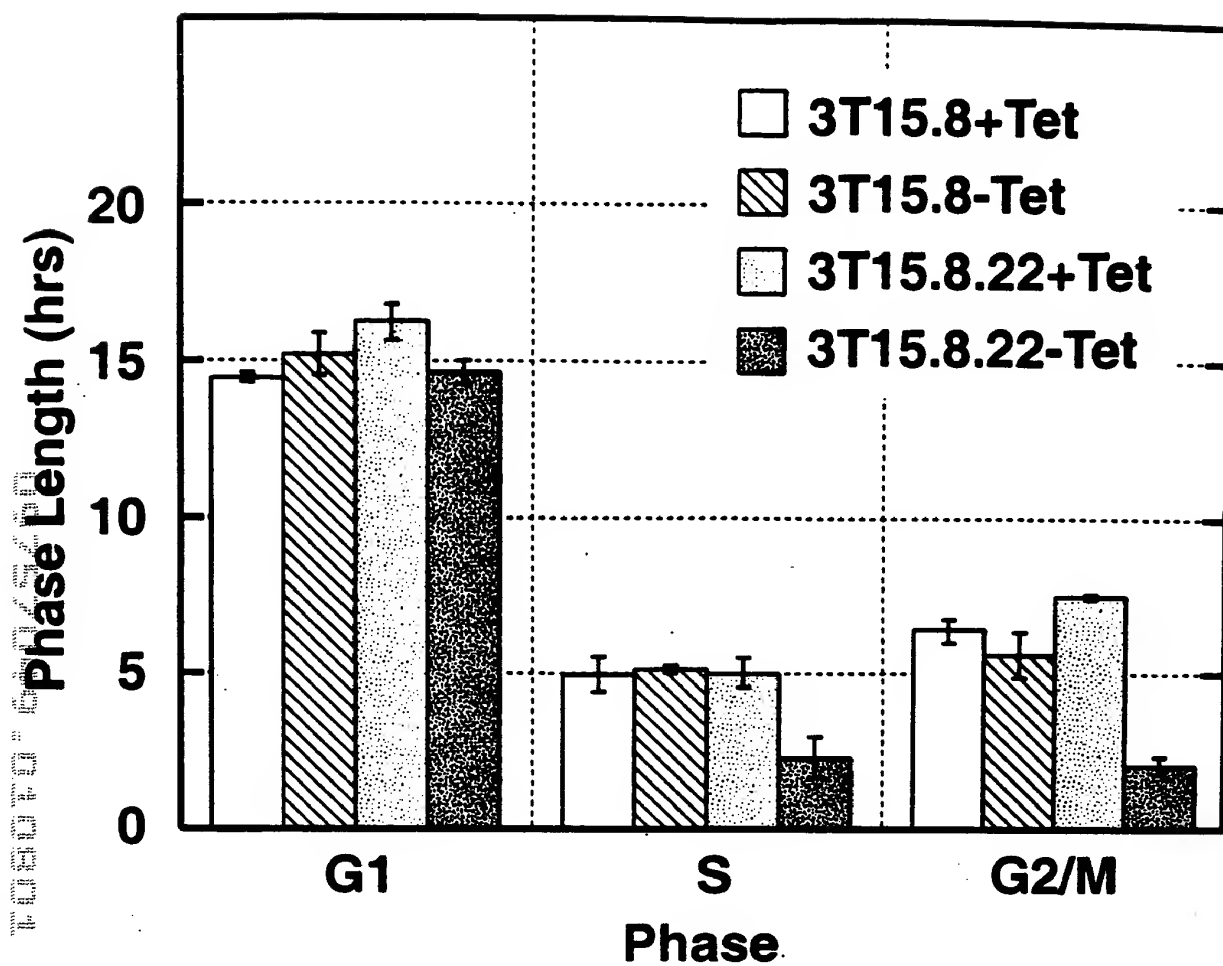


Fig. 7



**FIG. 8**

108010-0402560

Cell size by FSc  
(arbitrary units)

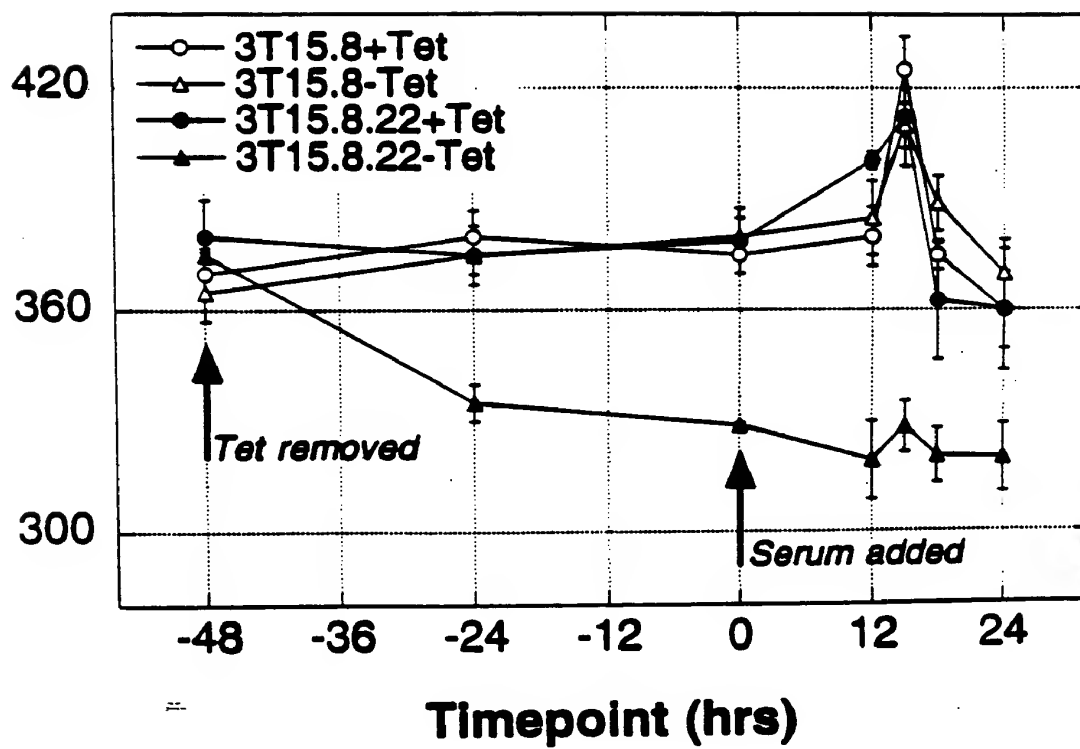
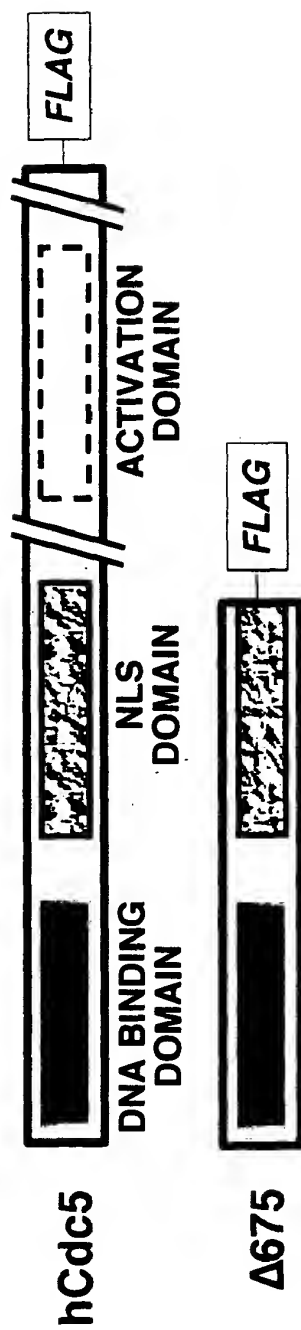


Fig. 9



**Fig. 10**

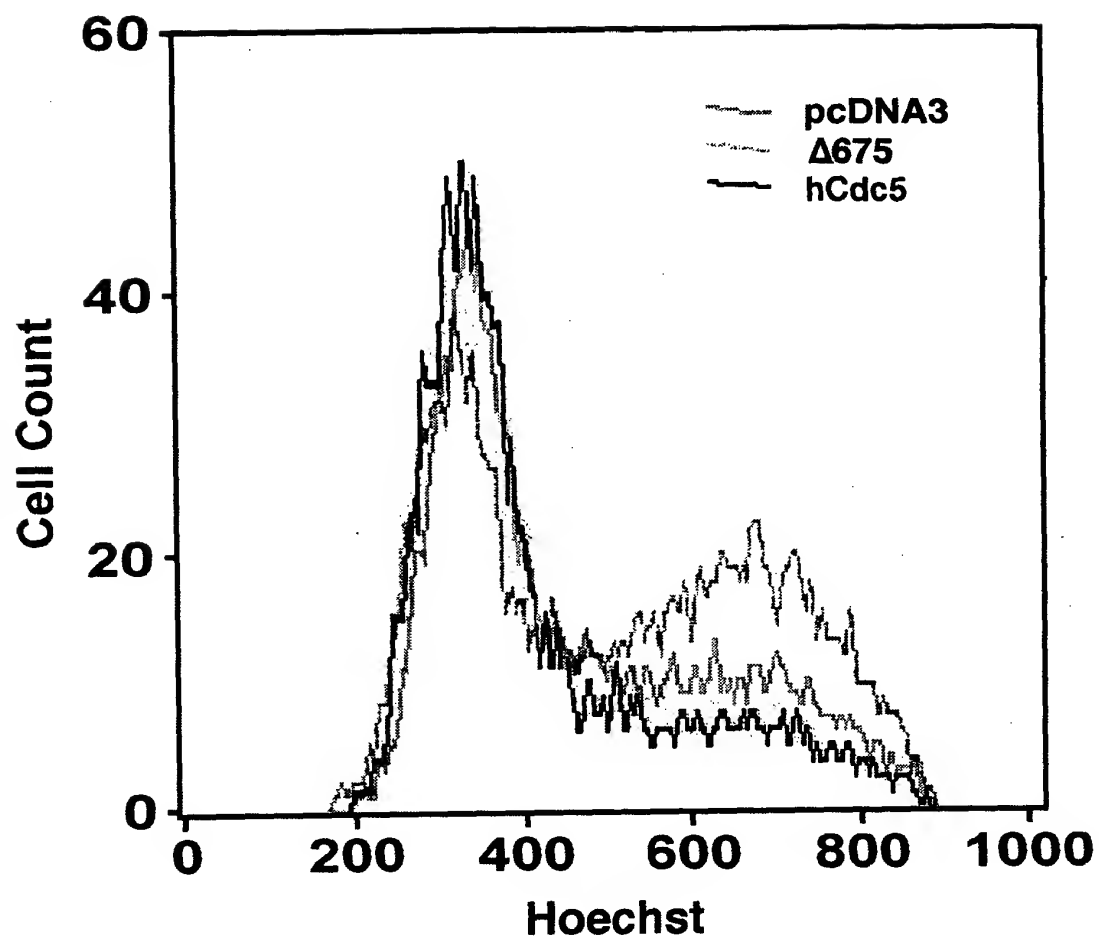


FIG. 11

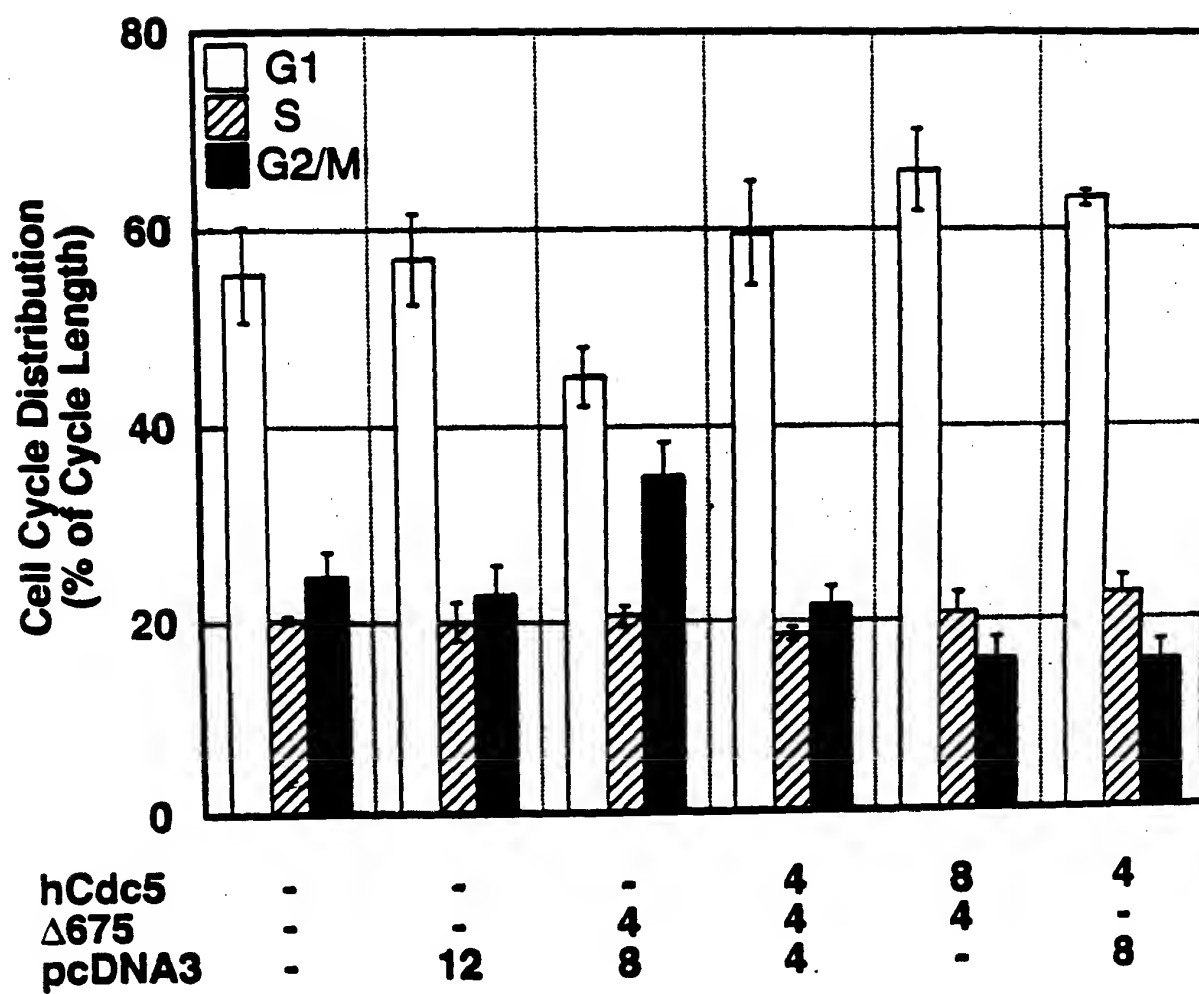


Fig. 12

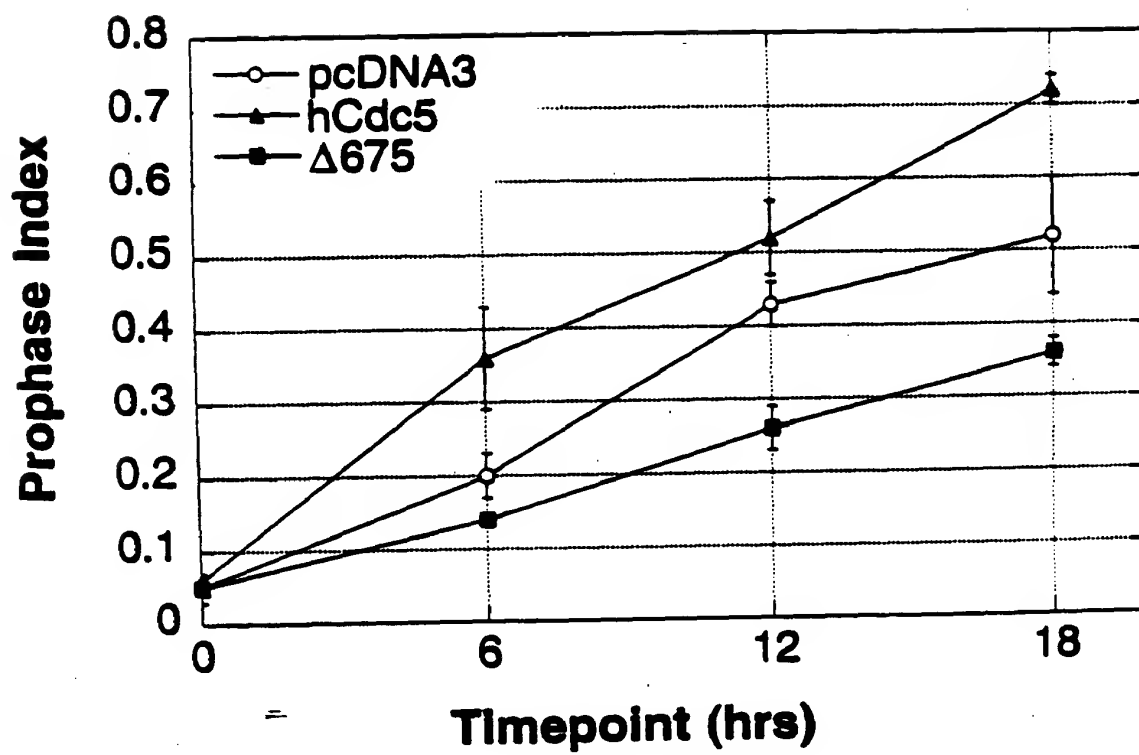


Fig. 13

0 12 15 18 21 hrs



**hCdc5**



**p50 CLNE**

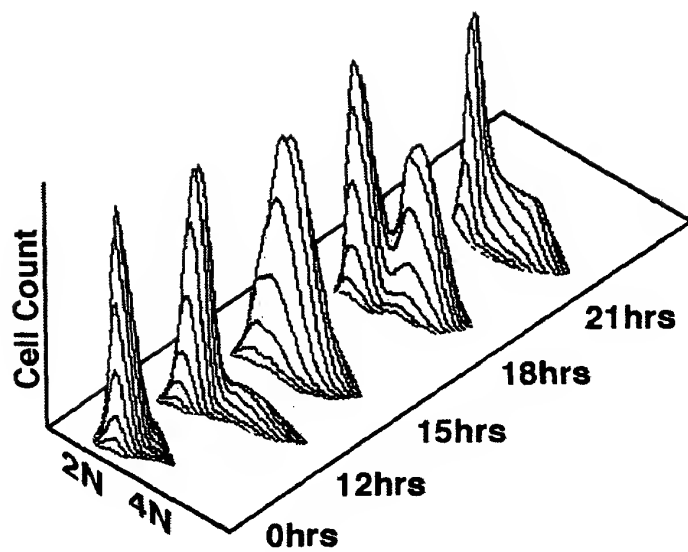


**p60 CLNA**



**p62 CLNB1**

**FIG. 14A**



**FIG. 14B**

Consensus G A T T T A A C A T A A (SEQ ID NO:13)

8.05 G A T T T A A C A T A A  
8.04 G A T T T A A C A T A A  
8.03 G A T T T A A C A T A A  
8.02 G A T T T A A C A T A A  
8.01 G A T T T A A C A T A A

6.05 G G T G T A A C G T G G (SEQ ID NO:36)  
6.04 G T G T T A C C A C A T (SEQ ID NO:37)  
6.03 C C A T A A A T T T A G (SEQ ID NO:38)  
6.02 G A G A T A A A G T C T (SEQ ID NO:39)  
6.01 G T G T T A T T G A A A (SEQ ID NO:40)

3.05 A C C C A C G T C T A T (SEQ ID NO:41)  
3.04 G G T T A G G A T A G G (SEQ ID NO:42)  
3.03 G T T G A G T A G T A T (SEQ ID NO:43)  
3.02 C T G T T A A T T T C C (SEQ ID NO:44)  
3.01 G G T G T T A T T G A T (SEQ ID NO:45)

FIG 15